==========
Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=2; day=1; hr=13; min=2; sec=58; ms=699;]
==========

Validated By CRFValidator v 1.0.3

Application No: 10552013 Version No: 4.0

Input Set:

Output Set:

Started: 2010-01-18 15:26:47.295
Finished: 2010-01-18 15:26:57.833
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 538 ms
Total Warnings: 103
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code		Error Description
W	402	Undefined organism found in <213> in SEQ ID (1)
W	402	Undefined organism found in <213> in SEQ ID (2)
W	402	Undefined organism found in <213> in SEQ ID (16)
W	402	Undefined organism found in <213> in SEQ ID (17)
W	402	Undefined organism found in <213> in SEQ ID (18)
W	402	Undefined organism found in <213> in SEQ ID (19)
W	402	Undefined organism found in <213> in SEQ ID (28)
W	402	Undefined organism found in <213> in SEQ ID (29)
W	402	Undefined organism found in <213> in SEQ ID (30)
W	402	Undefined organism found in <213> in SEQ ID (31)
W	402	Undefined organism found in <213> in SEQ ID (32)
W	402	Undefined organism found in <213> in SEQ ID (33)
W	402	Undefined organism found in <213> in SEQ ID (36)
W	402	Undefined organism found in <213> in SEQ ID (37)
W	213	Artificial or Unknown found in <213> in SEQ ID (52)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W	213	Artificial or Unknown found in <213> in SEQ ID (53)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W	213	Artificial or Unknown found in <213> in SEQ ID (54)

Input Set:

Output Set:

Started: 2010-01-18 15:26:47.295
Finished: 2010-01-18 15:26:57.833
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 538 ms
Total Warnings: 103
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code		Error Description
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W	213	Artificial or Unknown found in <213> in SEQ ID (55)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W	213	Artificial or Unknown found in <213> in SEQ ID (56)
W	213	Artificial or Unknown found in <213> in SEQ ID (60)
W	213	Artificial or Unknown found in <213> in SEQ ID (61)
W	213	Artificial or Unknown found in <213> in SEQ ID (62)
W	213	Artificial or Unknown found in <213> in SEQ ID (63)
W	213	Artificial or Unknown found in <213> in SEQ ID (64)
W	213	Artificial or Unknown found in <213> in SEQ ID (65)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W	213	Artificial or Unknown found in <213> in SEQ ID (66)
W	213	Artificial or Unknown found in <213> in SEQ ID (67)
W	213	Artificial or Unknown found in <213> in SEQ ID (68)
W	213	Artificial or Unknown found in <213> in SEQ ID (71)
W	213	Artificial or Unknown found in <213> in SEQ ID (75)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W	213	Artificial or Unknown found in <213> in SEQ ID (76)
E	224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W	213	Artificial or Unknown found in <213> in SEQ ID (77)

Input Set:

Output Set:

Started: 2010-01-18 15:26:47.295
Finished: 2010-01-18 15:26:57.833
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 538 ms
Total Warnings: 103
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
Sozer, Nursen
Frentzen, Margit
Bauer, Jorg
Keith, Stobart
Fraser, Thomas
Lazarus, Colin M
Qi, Baoxiu
Abbadi, Amine
Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013
<141> 2005-09-30

<150> PCT/EP2004/003224
<151> 2004-03-26

<150> DE103 14 759.4
<151> 2003-03-31

<150> DE103 48 996.7
<151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1
<211> 1047
<212> DNA
<213> Thraustochytrium

<220>
<221> CDS
<222> (38)..(952)
<223> LPAAT

<400> 1
gggcggtgtc cggccgttcg agcgcgtgga cgccaac atg agc gcg tgg acg agg 55
Met Ser Ala Trp Thr Arg
1 5

gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg 103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
10 15 20

ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc 151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
25 30 35

acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc 199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

```
    40                  45                  50
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc      247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                  60                  65                  70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg      295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                75                  80                  85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac      343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
            90                  95                  100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc      391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
        105                 110                 115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc      439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
    120                 125                 130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct      487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                 140                 145                 150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg      535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
                155                 160                 165
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag      583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
            170                 175                 180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag      631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
        185                 190                 195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg      679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
    200                 205                 210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac      727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                 220                 225                 230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag      775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                235                 240                 245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg      823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
            250                 255                 260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc      871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
        265                 270                 275
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga      919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
    280                 285                 290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca    972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                 300                 305
agcggtccag caacgggaga ttaaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa   1032
aaaaaaaaaa aaaaa                                                    1047
```

<210> 2
<211> 305
<212> PRT
<213> Thraustochytrium

<400> 2
Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
1 5 10 15
Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
20 25 30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
35 40 45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
50 55 60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65 70 75 80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
85 90 95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
100 105 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
115 120 125
Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
130 135 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145 150 155 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
165 170 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
180 185 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
195 200 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
210 215 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225 230 235 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
245 250 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
260 265 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
275 280 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
290 295 300
Leu
305

<210> 3
<211> 1701
<212> DNA
<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 3
ggcacgaggg aaattggctt tctatgtggc cgtacttatt cgaggaggtc aacgaaacaa 60
aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc 120
aactgaaaac ttgttttaat ttttttcttaa attgaaattc tgtgcctgaa agccaactct 180

```
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct    240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg    300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag    360
ggatatggat gttgtaaagg tgatttttgc aggtgataaa gtacctaagg agaaccgtgt    420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat    480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc    540
cttgtttggt tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt    600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg    660
gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtaccc atccatggct    720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca    780
agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta    840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga    900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact    960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag   1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt   1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg   1140
ctgtatgatc tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct   1200
ttccctgaca gtggaattga agagagccct ttgaacatag tggaaggtgt ttgcaatgtt   1260
gctctacacg tagtccttag cggttgggta ttctggtgct tgtttcattc ggtttggttg   1320
aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga   1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt   1440
agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaagggtga ggctcctctt   1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta   1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt   1620
ctcctttacc catcttgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc   1680
cccaaaaaaa aaaaaaaaaa a                                             1701
```

<210> 4
<211> 714
<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(714)
<223> LPAAT

<400> 4

```
atg gct ttg atg tat atc tgc aat ctt ctc tat aat ctg cat tta ttc       48
Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                  10                  15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc       96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat      144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa      192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt      240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac      288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
```

```
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta      336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
            100                 105                 110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca      384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115                 120                 125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat      432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
    130                 135                 140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca      480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg      528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta      576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
            180                 185                 190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc      624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                 200                 205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa      672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210                 215                 220
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa              714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235
```

<210> 5
<211> 237
<212> PRT
<213> Physcomitrella patens

<400> 5

```
Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                   10                  15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85                  90                  95
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
            100                 105                 110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115                 120                 125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
    130                 135                 140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                 170                 175
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
```

```
            180                 185                 190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                 200                 205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210                 215                 220
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                 230                 235
```

<210> 6
<211> 507
<212> DNA
<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 6
accaggtcga gatgcccatt attggactgt ttttgcaagc tttgcaaata atacccgtgg 60
accggactga tgctcagtct aggcaccatg cggctggcaa cgttcggcga agggctgtgg 120
acaatatgtg gtcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa 180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta 240
gataccctca caagtatgtc aacccctctt ggtgtgacca aggaggtccg ttggtcgttg 300
tgttgcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga 360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga 420
tggctaaagc gttaggcatc gtgtgcacag aacacagctt tctggatatt aagctagcgc 480
tggctgcaga aaagctcaaa cagcctt 507

<210> 7
<211> 1566
<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(1566)
<223> LPAAT

<400> 7
```
atg gag agc aca gca gat gtc gga atg tcc gac gac gat cct atc ctt       48
Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu
1               5                   10                  15
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa       96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc      144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
        35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg      192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
    50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg      240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc      288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                85                  90                  95
```

ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cgg ttc G 336